WHAT IS CLAIMED IS:

1. A method for destabilizing non-specific duplex formation between an oligonucleotide and a target nucleic acid, comprising an incubation of said target nucleic acid with a modified oligonucleotide, wherein said modified oligonucleotide comprises a homopolymeric sequence having a modification which decreases or abrogates hydrogen bonding between said modified oligonucleotide and non-specific target sequences.

2. The method of claim 1, wherein said modification is at least one universal base incorporated into said homopolymeric sequence.

3. The method of claim 2, wherein said universal base is 3-nitropyrrole.

4. The method of one of claims 1-3, wherein said oligonucleotide is a homopolymer comprising at least one nucleotide modification.

5. A method for increasing the proportion of full length cDNA clones in a library, comprising a use of a modified oligo d(T) during first strand synthesis, wherein said modified oligo d(T) comprises a modification which decreases or abrogates hydrogen bonding between said modified oligo d(T) and a non-specific target sequence, thereby increasing the proportion of full length cDNA clones.

6. The method of claim 5, wherein said modification is at least one universal base incorporated into said oligo d(T).

7. The method of claim 6, wherein said universal base is 3-nitropyrrole.

8. The method of claim 5, wherein said modification is at least one chemically modified nucleoside incorporated into said oligo d(T).

9. The method of claim 5, wherein said modification is at least one base analog incorporated into said oligo d(T).

10. The method of claim 9, wherein said base analog is inosine.

11. The method of claim 5, wherein said modification is at least one mismatch incorporated into said oligo d(T).

12. The method of claim 5, wherein said modification is a phosphate or ribose modification incorporated into said oligo d(T).

13. The method according to one of claims 5 to 12, wherein an enzyme capable of RNA-dependent DNA polymerization is used for said first strand synthesis.

14. The method according to one of claims 5 to 12, wherein an enzyme capable of RNA-dependent RNA polymerization is used for said first strand synthesis.

15. The method according to claim 14, wherein said enzyme is a reverse transcriptase selected from the group consisting of avian myoblastoid virus reverse transcriptase, murine moloney leukemia virus reverse transcriptase, and human immuno deficiency virus reverse transcriptase.

16. A kit for the synthesis of cDNA, said kit comprising a modified oligo d(T) primer, wherein said modified oligonucleotide includes a modification which decreases or abrogates hydrogen bonding between same and non-specific target sequences.

17. A method for reducing mispriming events during DNA synthesis comprising a use of a modified oligonucleotide to prime said DNA synthesis, wherein said modified oligonucleotide comprises a homopolymeric sequence having a modification which decreases or abrogates hydrogen bonding between said modified oligonucleotide and a non-specific target sequence, thereby reducing mispriming events, while maintaining a formation of a duplex with a *bona fide* homopolymeric target sequence.

18. The method of claim 17, wherein said modification is at least one universal base incorporated into said homopolymeric sequence.

19. The method of claim 18, wherein said universal base is 3-nitropyrrole.

20. The method of claims 17, 18 or 19, wherein said oligonucleotide is a homopolymer.

21. A method for reducing mispriming during 5' RACE comprising a use of a modified oligonucleotide to prime said 5' RACE, wherein said modified oligonucleotide comprises a homopolymeric sequence having a modification which decreases or abrogates hydrogen bonding between said modified oligonucleotide and a non-specific target sequence, thereby reducing mispriming events while maintaining a formation of a duplex with a *bona fide* homopolymeric target sequence.

22. The method of claim 21, wherein said modification is at least one universal base incorporated into said homopolymeric sequence.

23. The method of claim 21, wherein said universal base is 3-nitropyrrole.

24. The method of claim 21, wherein said modification is at least one chemically modified nucleoside incorporated into said homopolymeric sequence.

25. The method of claim 21, wherein said modification is at least one base analog incorporated into said homopolymeric sequence.

26. The method of claim 25, wherein said base analog is inosine.

27. The method of claim 21, wherein said modification is at least one mismatch incorporated into said homopolymeric sequence.

28. The method of claim 21, wherein said modification is a phosphate or ribose modification destabilizing mismatch recognition incorporated into said homopolymeric sequence.

29. A kit for 5' RACE comprising a modified oligonucleotide primer, comprising a homopolymeric sequence having a modification which decreases or abrogates hydrogen bonding between said modified oligonucleotide and non-specific target sequences.

30. A method for reducing mispriming during 3' RACE comprising a priming of said 3' RACE with a modified oligonucleotide, wherein said modified oligonucleotide comprises a homopolymeric sequence having a modification which decreases or abrogates hydrogen bonding between said modified oligonucleotide and a non-specific target sequence, thereby reducing mispriming events while maintaining a formation of a duplex with a *bona fide* homopolymeric target sequence.

31. The method of claim 30, wherein said modification is at least one universal base incorporated into said homopolymeric sequence.

32. A method for generating *bona fide* genetic markers comprising a use of a modified oligonucleotide to prime from homopolymeric stretches, wherein said modified oligonucleotide comprises a homopolymeric sequence having a modification which decreases or abrogates hydrogen bonding between said modified oligonucleotide and non-specific target sequences.

33. The method of claim 32, wherein said modified oligonucleotide primes from an internal A-rich region in an Alu repeat.

34. A method for stabilizing duplex formation between an oligonucleotide and a target homopolymeric sequence comprising an incubation of said target homopolymeric sequence with a modified oligonucleotide, wherein said modified oligonucleotide comprises a homopolymeric tract having a modification which decreases or abrogates hydrogen bonding between same and non-specific target sequences.

35. A method for reducing mispriming during sequencing comprising a use of a modified oligonucleotide to prime DNA synthesis, wherein said modified oligonucleotide comprises a homopolymeric sequence having a modification which decreases or abrogates hydrogen bonding between same and non-specific target sequences.

36. A method to improve the discrimination between a binding of an oligonucleotide sequence to its targetted homopolymeric sequence versus a non-homopolymeric tract comprising an insertion into a homopolymeric tract of said oligonucleotide sequence of at least one modification which decreases or abrogates hydrogen bonding between same and said non-homopolymeric tract.

37. A method for increasing the proportion of full length cDNA clones in a library, comprising a use of a modified oligonucleotide during second strand synthesis from a 3' end-tailed first strand product, wherein said modified oligonucleotide comprises a homopolymeric sequence having a modification which decreases or abrogates hydrogen bonding between said

modified oligo and a non-specific target sequence, thereby increasing the proportion of full length cDNA clones.